## Adding sample information

Twenty-five CEL files (samples) have been imported into Partek Genomics Suite. Sample information must be added to define the grouping and the goals of the experiment.

- Select Add Sample Attributes in the Import section of the Gene Expression workflow panel
- Choose the option Add Attributes from an Existing Column
- Select OK to open the Sample Information Creation dialog

In this tutorial, the file name (e.g., Down Syndrome-Astrocyte-748-Male-1-U133A.CEL) contains the information about a sample and is separated by hyphens (-). Choosing to split the file name by delimiters will separate the categories into different columns

 In the Sample Information panel, specify the column labels (Labels 1-4) as Type, Tissue, Subject, and Gender, set each as categorical, and set the other columns as skip (Figure 1). Select OK

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Please specify how y	ou want to split the colur	mn				
Choose to split your s	ample by delimiters or fixed	widths. Press the Update bu	tton to preview results.			
- Choose "By delimite	ers" if your fields are separa	ated by certain characters suc	h as commas or underscores.			
- Choose "By fixed y	vidths" if your fields are aligr	ned with fixed widths.				
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🗹 Hyphen ( - )		Width specification e	xample: 3, 5, 2			
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Figure 4. Configuring the Sample Information Creation dialog

- · A dialog window asking if you would like to save the spreadsheet with the new sample attribute will appear. Select Yes
- Make column 5. (Subject) random by right-clicking on the column header and selecting Properties from the pop-up menu (Figure 2).

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Figure 5. Changing column properties

• Select the Random Effect check box from the Properties dialog (Figure 3) then select OK.

Properties of Column 5 in Spreadsheet 1 ×						
Column La	abel:					
Subject						
Type:	categorical	✓ String Size: 7÷				
Attribute	: factor	✓ ✓ Random Effect				
		OK Cancel				

Figure 6. Setting column to Random Effect

The column 5. (Subject) will now be colored red, indicating that it is a random effect.

• To save changes to the spreadsheet, select the Save Active Spreadsheet icon (). Spreadsheets with unsaved changes have an asterisk next to their name in the spreadsheet tree.

Note: More details on Random vs. Fixed Effects can be found later in this tutorial under the section Identifying differentially expressed genes using ANOVA.

« Importing Affymetrix CEL files Exploring gene expression data »

## Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

